

ATTACHMENT A

<110> APPLICANT: Better, Marc D.
 Horwitz, Arnold H.
 <120> TITLE OF INVENTION: Human Engineered to Antibodies to Ep-CAM
 <130> FILE REFERENCE: 14923US02
 <140> CURRENT APPLICATION NUMBER: US/10/816,276
 <141> CURRENT FILING DATE: 2004-03-31
 <150> PRIOR APPLICATION NUMBER: 60/459,334
 <151> PRIOR FILING DATE: 2003-03-31
 <160> NUMBER OF SEQ ID NOS: 59
 <170> SOFTWARE: PatentIn version 3.2

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 <223> Mouse Human Chimeric Light Chain DNA and Protein
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ctc cta cat agt aat ggc atc act tat ttg tat tgg tat ctg cag aag	192
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys	
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tca gga gtc cca gac agg ttc agt agc agt ggg tca gga act gat ttc	288
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe	
65 70 75	
aca cty aga atc agc aga gtg gag gct gag gat gtg ggt gtt tat tac	336
Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr	
80 85 90	
tgt gct caa aat cta gaa ctt cct cgg acg ttc ggt gga ggc acc aag	384
Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gly Gly Thr Lys	
95 100 105	
ctt gag atg aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg	432
Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro	
110 115 120	
cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg	480
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu	
125 130 135 140	
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cct gga gag aca gtc aag atc tcc tgc aag gct tct gga tat acc ttc	144
Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe	
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aca aaa tat gga atg aac tgg gtg aag cag gct cca gga aag ggt tta	192
Thr Lys Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu	
30 35 40 45	
aag tgg atg ggc tgg ata aac acc tac act gaa gag cca aca tat ggt	240
Lys Trp Met Gly Trp Ile Asn Thr Tyr Thr Glu Glu Pro Thr Tyr Gly	
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gat gac ttc aag gga cgg ttt gcc ttc tct ttg gaa acc tct gcc agc	288
Asp Asp Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser	
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tat ttc tgt gca aga ttt ggc tct gct gtg gac tac tgg ggt caa gga	384
Tyr Phe Cys Ala Arg Phe Gly Ser Ala Val Asp Tyr Trp Gly Gln Gly	
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acc tcg gtc acc gtc tcc tca gcc agc aca aag ggc cca tcg gtc ttc	432
Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe	
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Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp	
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Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser	
175 180 185	
agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc	672
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro	
190 195 200 205	
agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt gac aaa	720
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210 215 220	
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Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro	
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Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser	

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Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp			
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Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys			
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acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc			1104
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Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu			
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Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu
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Val Thr Leu Gly Glu Ser Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
15                               20                               25
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Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
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cca ggg cag tct cct cag ctg ctc atc tat cag atg tct aac aga gcc      240
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
45                               50                               60
tca ggg gtc cca gac agg ttc agt agc agt gga tct ggg aca gat ttc      288
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
65                               70                               75
act ctc aag atc agc aga gtg gag gct gaa gat gtg gga gtt tat tac      336
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
80                               85                               90
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ctt gag atg aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg      432
Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
110                              115                              120
cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg      480
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
125                              130                              135
ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat      528
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
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agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa      624
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
175                              180                              185
gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag      672
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Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
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Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
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Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
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Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
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Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
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Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
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Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
      175      180      185
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-20      -15      -10      -5
gga tcc act gca gac atc gtg atg acc cag tct cca ctc tcc ctg cca      96
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro
      -1 1      5      10
gtc act cct gga gag ccg ggt tcc atc tcc tgc cgg tct agt aag agt      144
Val Thr Pro Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
      15      20      25
ctc cta cat agt aat ggc atc act tat ttg tat tgg tat ctg cag aaa      192
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Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Ser	Ser	Gly	Ser	Gly	Thr	Asp	Phe	
				65					70					75		
act	ctc	aag	atc	agc	aga	gtg	gag	gct	gaa	gat	gtg	gga	gtt	tat	tac	336
Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	
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tgt	gct	cag	aac	cta	gag	ctt	cca	cgg	acg	ttc	ggg	cag	ggc	acc	aag	384
Cys	Ala	Gln	Asn	Leu	Glu	Leu	Pro	Arg	Thr	Phe	Gly	Gln	Gly	Thr	Lys	
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ctt	gag	atg	aaa	cga	act	gtg	gct	gca	cca	tct	gtc	ttc	atc	ttc	ccg	432
Leu	Glu	Met	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	
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cca	tct	gat	gag	cag	ttg	aaa	tct	gga	act	gcc	tct	gtt	gtg	tgc	ctg	480
Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	
125						130				135					140	
ctg	aat	aac	ttc	tat	ccc	aga	gag	gcc	aaa	gta	cag	tgg	aag	gtg	gat	528
Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	
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aac	gcc	ctc	caa	tcg	ggg	aac	tcc	cag	gag	agt	gtc	aca	gag	cag	gac	576
Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	
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agc	aag	gac	agc	acc	tac	agc	ctc	agc	agc	acc	ctg	acg	ctg	agc	aaa	624
Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	
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Val	Thr	Pro	Gly	Glu	Pro	Gly	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Lys	Ser	
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Leu	Leu	His	Ser	Asn	Gly	Ile	Thr	Tyr	Leu	Tyr	Trp	Tyr	Leu	Gln	Lys	
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Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	
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Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu
125					130					135					140
Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp
				145					150					155	
Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp
		160						165					170		
Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys
	175						180					185			
Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln
	190					195					200				
Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys	
205					210						215				

<210> 9

<211> 88

<212> DNA

<213> Homo Sapiens

<220>

<221> misc_feature

<223> KL1 V Region Oligos Human Engineered ING-1 Light Chain (Kappa low)

<400> 9

tgctgacacc atgaggttct ctgctcagct tctggggctg cttgtgctct ggatccctgg	60
atccactgca gacatcgtga tgaccacg	88

<210> 10

<211> 85

<212> DNA

<213> Homo Sapiens

<220>

<221> misc_feature

<223> KL2 V Region Oligos Human Engineered ING-1 Light Chain (Kappa low)

<400> 10

actcttacta gaccggcagg agatgggaacc tgactctccc agagtgactg gattggagag	60
tgacagactgg gtcacacga tgtct	85

<210> 11

<211> 88

<212> DNA

<213> Homo Sapiens

<220>

<221> misc_feature

<223> KL3 V Region Oligos Human Engineered ING-1 Light Chain (Kappa low)

<400> 11

ctgccgggtct agtaagagtc tctacatag taatggcatc acttatttgt attggtatct	60
gcagaaacca gggcagctc ctcagctg	88

<210> 12

<211> 86

<212> DNA

<213> Homo Sapiens

<220>

<221> misc_feature

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<223> KL4 V Region Oligos Human Engineered ING-1 Light Chain (Kappa
low)
<400> 12
tgtcccagat ccaactgctac tgaacctgtc tgggaccctt gaggtctgtg tagacatctg
atagatgagc agctgaggag actgcc
60
86

<210> 13
<211> 77
<212> DNA
<213> Homo Sapiens
<220>
<221> misc_feature
<223> KL5 V Region Oligos Human Engineered ING-1 Light Chain (Kappa
low)
<400> 13
agcagtggat ctgggacaga ttctactctc aagatcagca gactggaggc tgaagatgtg
ggagtttatt actgtgc
60
77

<210> 14
<211> 75
<212> DNA
<213> Homo Sapiens
<220>
<221> misc_feature
<223> KL6 V Region Oligos Human Engineered ING-1 Light Chain (Kappa
low)
<400> 14
tttgatttca agcttggtgc cctgaccgaa cgtccgtgga agctctaggt tctgagcaca
gtaataaact cccac
60
75

<210> 15
<211> 22
<212> DNA
<213> Homo Sapiens
<220>
<221> misc_feature
<223> Low Risk Primers Forward Primer: KF ING-1 Light Chain Oligos
<400> 15
ttatgtcgac accatgaggt tc
22

<210> 16
<211> 21
<212> DNA
<213> Homo Sapiens
<220>
<221> misc_feature
<223> Low risk Primers Reverse Primer: KR ING-1 Light Chain Oligos
<400> 16
tttgatttca agcttggtgc c
21

<210> 17
<211> 85
<212> DNA
<213> Homo Sapiens
<220>
<221> misc_feature
<223> Moderate Risk Primer: KM2 V Region Oligos Human Engineered ING-1

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Light Chain Oligos (Kappa Moderate)

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<400> 17
actcttacta gaccggcagg agatggaacc cggctctcca ggagtgactg gcagggagag 60
tggagactgg gtcacacga tgtct 85

<210> 18
<211> 1398
<212> DNA
<213> Homo Sapiens
<220>
<221> misc_feature
<223> Low Risk Human Engineered ING-1 Heavy Chain (HC)
<220>
<221> misc_feature
<223> Variable region of HC is Amino Acids is 1-116
<220>
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<222> (1)..(1395)
<220>
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<222> (58)..()
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Met Ala Trp Val Ser Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser
-15 -10 -5
gcc caa gca cag atc cag ttg gtg cag tct gga cct gag gtg aag aag 96
Ala Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Val Lys Lys
-1 1 5 10
cct gga gag tcc gtc aag atc tcc tgc aag gct tct gga tat acc ttc 144
Pro Gly Glu Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
15 20 25
aca aaa tat gga atg aac tgg gtg aag cag gct cca gga cag ggt tta 192
Thr Lys Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Gln Gly Leu
30 35 40 45
aag tgg atg ggc tgg ata aac acc tac act gaa gag cca aca tat ggt 240
Lys Trp Met Gly Trp Ile Asn Thr Tyr Thr Glu Glu Pro Thr Tyr Gly
50 55 60
gat gac ttc aag gga cgg ttt acc ttc acc ttg gac acc tct act agc 288
Asp Asp Phe Lys Gly Arg Phe Thr Phe Thr Leu Asp Thr Ser Thr Ser
65 70 75
act gcc tat ttg gaa atc tct tct ctc cgg agt gag gac acg gct aca 336
Thr Ala Tyr Leu Glu Ile Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr
80 85 90
tat ttc tgt gca aga ttt ggc tct gct gtg gac tac tgg ggt caa gga 384
Tyr Phe Cys Ala Arg Phe Gly Ser Ala Val Asp Tyr Trp Gly Gln Gly
95 100 105
acc ttg gtc acc gtc tcc tca gcc agc aca aag ggc cca tcg gtc ttc 432
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
110 115 120 125
ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg 480
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
130 135 140
ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg 528
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155
aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta 576
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu

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160	165	170	
cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc			624
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser			
175	180	185	
agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc			672
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro			
190	195	200	205
agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt gac aaa			720
Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys			
210	215	220	
act cac aca tgc cca cgc tgc cca gca cct gaa ctc ctg ggg gga ccg			768
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro			
225	230	235	
tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc			816
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser			
240	245	250	
cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac			864
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp			
255	260	265	
cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat			912
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn			
270	275	280	285
gcc aag aca aag cgc cgg gag gag cag tac aac agc acg tac cgg gtg			960
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val			
290	295	300	
gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag			1008
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu			
305	310	315	
tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa			1056
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys			
320	325	330	
acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc			1104
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr			
335	340	345	
ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc ctg acc			1152
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr			
350	355	360	365
tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag			1200
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu			
370	375	380	
agc aat ggg cag cgc gag aac aac tac aag acc acg cct ccc gtg ctg			1248
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu			
385	390	395	
gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag			1296
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys			
400	405	410	
agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag			1344
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu			
415	420	425	
gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt			1392
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly			
430	435	440	445
aaa tga			1398
Lys			

<210> 19

<211> 465

<212> PRT

<213> Homo Sapiens

<400> 19

Met Ala Trp Val Ser Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser
-15 -10 -5
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-1 1 5 10
Pro Gly Glu Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
15 20 25
Thr Lys Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Gln Gly Leu
30 35 40 45
Lys Trp Met Gly Trp Ile Asn Thr Tyr Thr Glu Glu Pro Thr Tyr Gly
50 55 60
Asp Asp Phe Lys Gly Arg Phe Thr Phe Thr Leu Asp Thr Ser Thr Ser
65 70 75
Thr Ala Tyr Leu Glu Ile Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr
80 85 90
Tyr Phe Cys Ala Arg Phe Gly Ser Ala Val Asp Tyr Trp Gly Gln Gly
95 100 105
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
110 115 120 125
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
130 135 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
160 165 170
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
175 180 185
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
190 195 200 205
Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys
210 215 220
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225 230 235
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
240 245 250
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
255 260 265
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
270 275 280 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
290 295 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305 310 315
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
320 325 330
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
335 340 345
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
350 355 360 365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385 390 395
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Lys
400 405 410

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 415 420 425
 Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 430 435 440 445
 Lys

<210> 20
 <211> 1398
 <212> DNA
 <213> Homo Sapiens
 <220>
 <221> misc_feature
 <223> Low + Moderate Risk Human Engineered ING-1 Heavy Chain (HC)
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atg gct tgg gtg tcc acc ttg cta ttc ctg atg gca gct gcc caa agt	48
Met Ala Trp Val Ser Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser	
-15 -10 -5	
gcc caa gca cag atc cag ttg gtg cag tct gga gct gag gtg aag aag	96
Ala Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys	
-1 1 5 10	
cct gga gag tca gtc aag atc tcc tgc aag gct tct gga tat acc ttc	144
Pro Gly Glu Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe	
15 20 25	
aca aaa tat gga atg aac tgg gtg cga cag gct cca gga caa ggt tta	192
Thr Lys Tyr Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu	
30 35 40 45	
gag tgg atg ggc tgg ata aac acc tac act gaa gag cca aca tat ggt	240
Glu Trp Met Gly Trp Ile Asn Thr Tyr Thr Glu Glu Pro Thr Tyr Gly	
50 55 60	
cag aag ttc cag gga cgg ttt acc ttc acc ttg gac acc tct act agc	288
Gln Lys Phe Gln Gly Arg Phe Thr Phe Thr Leu Asp Thr Ser Thr Ser	
65 70 75	
act gcc tat ttg gaa atc tct tcg ctc cgg agt gag gac acg gct gtg	336
Thr Ala Tyr Leu Glu Ile Ser Ser Leu Arg Ser Glu Asp Thr Ala Val	
80 85 90	
tat ttc tgt gca aga ttt ggc tct gct gtg gac tac tgg ggt cca gga	384
Tyr Phe Cys Ala Arg Phe Gly Ser Ala Val Asp Tyr Trp Gly Gln Gly	
95 100 105	
acc ttg gtc acc gtc tcc tca gcc agc aca aag ggc cca tcg gtc ttc	432
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe	
110 115 120 125	
ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg	480
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu	
130 135 140	
ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg	528
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp	
145 150 155	
aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta	576
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu	
160 165 170	
cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc	624

Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser		
	175					180				185							
agc	agc	ttg	ggc	acc	cag	acc	tac	atc	tgc	aac	gtg	aat	cac	aag	ccc	672	
Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro		
190					195				200						205		
agc	aac	acc	aag	gtg	gac	aag	aga	gtt	gag	ccc	aaa	tct	tgt	gac	aaa	720	
Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys		
			210						215					220			
act	cac	aca	tgc	cca	ccg	tgc	cca	gca	cct	gaa	ctc	ctg	ggg	gga	ccg	768	
Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro		
			225						230					235			
tca	gtc	ttc	ctc	ttc	ccc	cca	aaa	ccc	aag	gac	acc	ctc	atg	atc	tcc	816	
Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser		
			240						245								
cgg	acc	cct	gag	gtc	aca	tgc	gtg	gtg	gtg	gac	gtg	agc	cac	gaa	gac	864	
Arg	Thr	Pro	Glu	Thr	Cys	Val	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp		
			255						260					265			
cct	gag	gtc	aag	ttc	aac	tgg	tac	gtg	gac	ggc	gtg	gag	gtg	cat	aat	912	
Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn		
			270						280						285		
gcc	aag	aca	aag	ccg	cgg	gag	gag	cag	tac	aac	agc	acg	tac	cgg	gtg	960	
Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val		
			290						295					300			
gtc	agc	gtc	ctc	acc	gtc	ctg	cac	cag	gac	tgg	ctg	aat	ggc	aag	gag	1008	
Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu		
			305						310					315			
tac	aag	tgc	aag	gtc	tcc	aac	aaa	gcc	ctc	cca	gcc	ccc	atc	gag	aaa	1056	
Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys		
			320						325					330			
acc	atc	tcc	aaa	gcc	aaa	ggg	cag	ccc	cga	gaa	cca	cag	gtg	tac	acc	1104	
Thr	Ile	Ser	Lys	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Thr		
			335						340					345			
ctg	ccc	cca	tcc	cgg	gat	gag	ctg	acc	aag	aac	cag	gtc	agc	ctg	acc	1152	
Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr		
			350						355					365			
tgc	ctg	gtc	aaa	ggc	ttc	tat	ccc	agc	gac	atc	gcc	gtg	gag	tgg	gag	1200	
Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu		
			370						375					380			
agc	aat	ggg	cag	ccg	gag	aac	aac	tac	aag	acc	acg	cct	ccc	gtg	ctg	1248	
Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu		
			385						390					395			
gac	tcc	gac	ggc	tcc	ttc	ttc	ctc	tac	agc	aag	ctc	acc	gtg	gac	aag	1296	
Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys		
			400						405					410			
agc	agg	tgg	cag	cag	ggg	aac	gtc	ttc	tca	tgc	tcc	gtg	atg	cat	gag	1344	
Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu		
			415						420					425			
gct	ctg	cac	aac	cac	tac	acg	cag	aag	agc	ctc	tcc	ctg	tct	ccg	ggg	1392	
Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly		
			430						435					440			
aaa	tga													445			
Lys																1398	

<210> 21
 <211> 465
 <212> PRT
 <213> Homo Sapiens

<400> 21

Met	Ala	Trp	Val	Ser	Thr	Leu	Leu	Phe	Leu	Met	Ala	Ala	Ala	Gln	Ser	-15	-10	-5
Ala	Gln	Ala	Gln	Ile	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	-1	1	5
Pro	Gly	Glu	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	15	20	25
Thr	Lys	Tyr	Gly	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	30	35	40
Glu	Trp	Met	Gly	Trp	Ile	Asn	Thr	Tyr	Thr	Glu	Glu	Pro	Thr	Tyr	Gly	50	55	60
Gln	Lys	Phe	Gln	Gly	Arg	Phe	Thr	Phe	Thr	Leu	Asp	Thr	Ser	Thr	Ser	65	70	75
Thr	Ala	Tyr	Leu	Glu	Ile	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	80	85	90
Tyr	Phe	Cys	Ala	Arg	Phe	Gly	Ser	Ala	Val	Asp	Tyr	Trp	Gly	Gln	Gly	95	100	105
Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	110	115	120
Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	130	135	140
Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	145	150	155
Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	160	165	170
Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	175	180	185
Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	190	195	200
Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	210	215	220
Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	225	230	235
Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	240	245	250
Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	255	260	265
Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	270	275	280
Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	290	295	300
Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	305	310	315
Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	320	325	330
Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	335	340	345
Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	350	355	360
Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	370	375	380
Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	385	390	395
Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	400	405	410
Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	415	420	425

Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly
430					435				440					445	
Lys															

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<210> 22
<211> 91
<212> DNA
<213> HomoSapiens
<220>
<221> misc_feature
<223> GL1 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos
      (gamma low)
<400> 22
      tgtcgacacc atggcttggg tgtccacctt gctattcctg atggcagctg cccaaagtgc      60
      ccaagcacag atccagtgg tgcagtctgg a                                     91

<210> 23
<211> 90
<212> DNA
<213> HomoSapiens
<220>
<221> misc_feature
<223> GL2 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos
      (gamma low)
<400> 23
      atattttgtg aaggtatata cagaagcctt gcaggagata ttgacggact ctccaggctt      60
      cttcacctca ggtccagact gcaccaactg                                     90

<210> 24
<211> 91
<212> DNA
<213> HomoSapiens
<220>
<221> misc_feature
<223> GL3 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos
      (gamma low)
<400> 24
      tggatatacc ttcacaaaat atggaatgaa ctgggtgaag caggctccag gacagggttt      60
      aaagtggatg ggctggataa acacctacac t.                                     91

<210> 25
<211> 90
<212> DNA
<213> HomoSapiens
<220>
<221> misc_feature
<223> GL4 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos
      (gamma low)
<400> 25
      cagtgctagt agaggtgtcc aaggtgaagg taaaccgtcc cttgaagtca tcaccatatg      60
      ttggtctctc agtgtaggtg tttatccagc                                     90

<210> 26
<211> 90
<212> DNA
<213> HomoSapiens
<220>

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<221> misc_feature
<223> GL5 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos
(gamma low)
<400> 26
gacacctcta ctgacctgc ctatttggaa atctcttctc tccggagtga ggacacggct 60
acatatctct gtgcaagatt tggctctgct 90

<210> 27
<211> 85
<212> DNA
<213> HomoSapiens
<220>
<221> misc_feature
<223> GL6 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos
(gamma low)
<400> 27
gaccgatggg ccttttgtgc tggctgagga gacggtgacc aaggttcctt gaccccagta 60
gtcccacagca gagccaaatc ttgca 85

<210> 28
<211> 22
<212> DNA
<213> HomoSapiens
<220>
<221> misc_feature
<223> Human Engineered ING-1 Heavy Chain Oligos-Low Risk Primers
Forward primer:GF
<400> 28
ttatgtcgac accatggcct gg 22

<210> 29
<211> 17
<212> DNA
<213> HomoSapiens
<220>
<221> misc_feature
<223> Human Engineered ING-1 Heavy Chain Oligos Low Risk Primers
-Reverse Primer GR
<220>
<221> misc_feature
<223> ING-1 Heavy Chain Oligos Low Risk Primers Reverse Primer GR
<400> 29
gaccgatggg ccttttg 17

<210> 30
<211> 90
<212> DNA
<213> HomoSapiens
<220>
<221> misc_feature
<223> GM2 V Region Oligos Human Engineered ING-1 Heavy Chain Oligos-Low
+ Moderate Risk Primers
<400> 30
atattttgtg aaggtatatc cagaagcctt gcaggagatc ttgactgact ctccaggctt 60
cttcacctca gctccagact gcaccaactg 90

<210> 31

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<211> 91
<212> DNA
<213> HomoSapiens
<220>
<221> misc_feature
<223> GM3 V Region Oligos Human Engineered ING-1 Heavy Chain Oligos-Low
+ Moderate Risk Primers
<400> 31
tggatatacc ttcacaaaat atggaatgaa ctgggtgcga caggctccag gacaaggttt      60
agagtggatg ggctggataa acacctacac t                                     91

<210> 32
<211> 90
<212> DNA
<213> HomoSapiens
<220>
<221> misc_feature
<223> GM4 V Region Oligos Human Engineered ING-1 Heavy Chain Oligos-Low
+ Moderate Risk Primers
<400> 32
cagtgctagt agagggtgcc aagggtgaagg taaaccgtcc ctggaacttc tgaccatatg      60
ttggctcttc agtgtaggty ttatccagc                                     90

<210> 33
<211> 90
<212> DNA
<213> HomoSapiens
<220>
<221> misc_feature
<223> GM5 V Region Oligos Human Engineered ING-1 Heavy Chain Oligos-Low
+ Moderate Risk Primers
<400> 33
gacacctcta ctagcactgc ctatttggaa atctcttcgc tccggagtga ggacacggct      60
gtgtatttct gtgcaagatt tggctctgct                                     90

<210> 34
<211> 720
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
<223> P1=P Human Engineered (low risk) ING1 light Chain with one
moderate risk proline change; proline at position 8 (P1)
<220>
<221> CDS
<222> (1)..(717)
<220>
<221> mat_peptide
<222> (61)..()
<400> 34
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Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
-20 -15 -10 -5
gga tcc act gca gac atc gtg atg acc cag tct cca ctc tcc aat cca      96
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Pro Leu Ser Asn Pro
-1 1 5 10
gtc act ctg gga gag tca ggt tcc atc tcc tgc cgg tct agt aag agt      144

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ctt gag atg aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg	432
Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro	
110 115 120	
cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg	480
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu	
125 130 135 140	
ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat	528
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp	
145 150 155	
aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac	576
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp	
160 165 170	
agc aag gac agc acc tac agc ctc agc acc ctg acg ctg agc aaa	624
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys	
175 180 185	
gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag	672
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln	
190 195 200	
ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag	720
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys	
205 210 215	

<210> 37

<211> 239

<212> PRT

<213> Homo sapiens

<400> 37

Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro	
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Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Ala Leu Ser Asn Pro	
-1 1 5 10	
Val Thr Pro Gly Glu Ser Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser	
15 20 25	
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys	
30 35 40	
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala	
45 50 55 60	
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe	
65 70 75	
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr	
80 85 90	
Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys	
95 100 105	
Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro	
110 115 120	
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu	
125 130 135 140	
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp	
145 150 155	
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp	
160 165 170	
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys	
175 180 185	
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln	
190 195 200	
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys	
205 210 215	

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<210> 38
<211> 720
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
<223> P3=P Human Engineered (low risk) ING1 light Chain with one
moderate risk proline change; proline at position 18 (P3)
<220>
<221> CDS
<222> (1)..(717)
<220>
<221> mat_peptide
<222> (61)..()
<400> 38
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Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
-20                               -15                               -10                               -5
gga tcc act gca gac atc gtg atg acc cag tct gca ctc tcc aat cca      96
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Ala Leu Ser Asn Pro
-1 1                               5                               10
gtc act ctg gga gag ccg ggt tcc atc tcc tgc cgg tct agt aag agt      144
Val Thr Leu Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
15                               20                               25
ctc cta cat agt aat ggc atc act tat ttg tat tgg tat ctg cag aaa      192
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
30                               35                               40
cca ggg cag tct cct cag ctg ctc atc tat cag atg tct aac aga gcc      240
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
45                               50                               55                               60
tca ggg gtc cca gac agg ttc agt agc agt gga tct ggg aca gat ttc      288
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
65                               70                               75
act ctc aag atc agc aga gtg gag gct gaa gat gtg gga gtt tat tac      336
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
80                               85
tgt gct cag aac cta gag ctt ccg cgg acg ttc ggt cag ggc acc aag      384
Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
95                               100                               105
ctt gag atg aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg      432
Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
110                               115                               120
cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg      480
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
125                               130                               135                               140
ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat      528
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
145                               150                               155
aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac      576
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
160                               165                               170
agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa      624
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
175                               180                               185
gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag      672
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln

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190          195          200
ggc ctg agc tgc ccc gtc aca aag agc ttc aac agg gga gag tgt tag
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
205          210          215

<210> 39
<211> 239
<212> PRT
<213> Homo sapiens
<400> 39
Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
-20          -15          -10          -5
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Ala Leu Ser Asn Pro
          -1 1          5          10
Val Thr Leu Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
          15          20          25
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
          30          35          40
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
          45          50          55          60
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
          65          70          75
Thr Leu Lys Ile Ser Arg Val Glu Ala Asp Val Gly Val Tyr Tyr
          80          85          90
Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
          95          100          105
Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
          110          115          120
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
          125          130          135          140
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
          145          150          155
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
          160          165          170
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
          175          180          185
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
          190          195          200
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
205          210          215

<210> 40
<211> 720
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
<223> P1P2=Human Engineered (low risk) ING1 light Chain with one
moderate risk proline change; proline at position 8 (P1) 15(P2)
<220>
<221> CDS
<222> (1)..(717)
<220>
<221> mat_peptide
<222> (61)..()
<400> 40
atg agg ttc tct gct cag ctt ctg ggg ctg ctt gtg ctc tgg atc cct

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Met	Arg	Phe	Ser	Ala	Gln	Leu	Leu	Gly	Leu	Leu	Val	Leu	Trp	Ile	Pro		
-20					-15				-10						-5		
gga	tcc	act	gca	gac	atc	gtg	atg	acc	cag	tct	cca	ctc	tcc	aat	cca	96	
Gly	Ser	Thr	Ala	Asp	Ile	Val	Met	Thr	Gln	Ser	Pro	Leu	Ser	Asn	Pro		
			-1	1				5				10					
gtc	act	cct	gga	gag	tca	ggt	tcc	atc	tcc	tgc	cgg	tct	agt	aag	agt	144	
Val	Thr	Pro	Gly	Glu	Ser	Gly	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Ser	Lys		
		15				20			25								
ctc	cta	cat	agt	aat	ggc	atc	act	tat	tgt	tat	tgg	tat	ctg	cag	aaa	192	
Leu	Leu	His	Ser	Asn	Gly	Ile	Thr	Tyr	Leu	Tyr	Trp	Tyr	Leu	Gln	Lys		
	30					35			40								
cca	ggg	cag	tct	cct	cag	ctg	ctc	atc	tat	cag	atg	tct	aac	aga	gcc	240	
Pro	Gly	Gln	Ser	Pro	Gln	Leu	Leu	Ile	Tyr	Gln	Met	Ser	Asn	Arg	Ala		
45					50				55					60			
tca	ggg	gtc	cca	gac	agg	ttc	agt	agc	agt	gga	tct	ggg	aca	gat	ttc	288	
Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Ser	Ser	Gly	Ser	Gly	Thr	Asp	Phe		
			65					70				75					
act	ctc	aag	atc	agc	aga	gtg	gag	gct	gaa	gat	gtg	gga	gtt	tat	tac	336	
Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr		
		80					85					90					
tgt	gct	cag	aac	cta	gag	ctt	ccg	cgg	acg	ttc	ggt	cag	ggc	acc	aag	384	
Cys	Ala	Gln	Asn	Leu	Glu	Leu	Pro	Arg	Thr	Phe	Gly	Gln	Gly	Thr	Lys		
		95				100					105						
ctt	gag	atg	aaa	cga	act	gtg	gct	gca	cca	tct	gtc	ttc	atc	ttc	ccg	432	
Leu	Glu	Met	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro		
	110				115						120						
cca	tct	gat	gag	cag	ttg	aaa	tct	gga	act	gcc	tct	gtt	gtg	tgc	ctg	480	
Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu		
125					130				135					140			
ctg	aat	aac	ttc	tat	ccc	aga	gag	gcc	aaa	gta	cag	tgg	aag	gtg	gat	528	
Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp		
			145				150					155					
aac	gcc	ctc	caa	tcg	ggg	aac	tcc	cag	gag	agt	gtc	aca	gag	cag	gac	576	
Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp		
		160				165					170						
agc	aag	gac	agc	acc	tac	agc	ctc	agc	agc	acc	ctg	acg	ctg	agc	aaa	624	
Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys		
		175				180					185						
gca	gac	tac	gag	aaa	cac	aaa	gtc	tac	gcc	tgc	gaa	gtc	acc	cat	cag	672	
Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln		
	190				195				200								
ggc	ctg	agc	tcg	ccc	gtc	aca	aag	agc	ttc	aac	agg	gga	gag	tgt	tag	720	
Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys			
205					210				215								

<210> 41

<211> 239

<212> PRT

<213> Homo sapiens

<400> 41

Met	Arg	Phe	Ser	Ala	Gln	Leu	Leu	Gly	Leu	Leu	Val	Leu	Trp	Ile	Pro		
-20					-15				-10						-5		
Gly	Ser	Thr	Ala	Asp	Ile	Val	Met	Thr	Gln	Ser	Pro	Leu	Ser	Asn	Pro		
			-1	1				5				10					
Val	Thr	Pro	Gly	Glu	Ser	Gly	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Lys	Ser		
		15				20			25								
Leu	Leu	His	Ser	Asn	Gly	Ile	Thr	Tyr	Leu	Tyr	Trp	Leu	Gln	Lys			

30	35	40	
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala			
45	50	55	60
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe			
	65	70	75
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr			
	80	85	90
Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys			
	95	100	105
Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro			
	110	115	120
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu			
	125	130	135
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp			
	145	150	155
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp			
	160	165	170
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys			
	175	180	185
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln			
	190	195	200
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys			
205	210	215	

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<210> 42
<211> 720
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
<223> P1P3= Human Engineered (low risk) INGI light Chain with one
moderate risk proline change; proline at position 8 (P1) 18 (P3)
<220>
<221> CDS
<222> (1)..(717)
<220>
<221> mat_peptide
<222> (61)..()
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    Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
    -20      -15      -10      -5
    gga tcc act gca gac atc gtg atg acc cag tct cca ctc tcc aat cca      96
    Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Pro Leu Ser Asn Pro
    -1  1      5      10
    gtc act ctg gga gag ccg ggt tcc atc tcc tgc cgg tct agt aag agt      144
    Val Thr Leu Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Lys Ser
    15      20      25
    ctc cta cat agt aat ggc atc act tat ttg tat tgg tat ctg cag aaa      192
    Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
    30      35      40
    cca ggg cag tct cct cag ctg ctc atc tat cag atg tct aac aga gcc      240
    Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
    45      50      55      60
    tca ggg gtc cca gac agg ttc agt agc agt gga tct ggg aca gat ttc      288
    Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
    65      70      75

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act ctc aag atc agc aga gtg gag gct gaa gat gtg gga gtt tat tac	336
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr	
80 85 90	
tgt gct cag aac cta gag ctt ccg cgg acg ttc ggt cag ggc acc aag	384
Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys	
95 100 105	
ctt gag atg aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg	432
Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro	
110 115 120	
cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg	480
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Cys Leu	
125 130 135 140	
ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat	528
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp	
145 150 155	
aac gcc ctc caa tcg ggt aac tcc gag gag agt gtc aca gag cag gac	576
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp	
160 165 170	
agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa	624
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys	
175 180 185	
gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag	672
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln	
190 195 200	
ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag	720
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys	
205 210 215	

<210> 43

<211> 239

<212> PRT

<213> Homo sapiens

<400> 43

Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro	
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-1 1 5 10	
Val Thr Leu Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser	
15 20 25	
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys	
30 35 40	
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala	
45 50 55 60	
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe	
65 70 75	
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr	
80 85 90	
Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys	
95 100 105	
Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro	
110 115 120	
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu	
125 130 135 140	
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp	
145 150 155	
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp	
160 165 170	

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
 175 180 185
 Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
 190 195 200
 Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 205 210 215

<210> 44
 <211> 720
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> misc_feature
 <223> P2P3=Human Engineered (low risk) ING1 light Chain with one
 moderate risk proline change; proline at position 8 (P1) 18 (P3)

<220>
 <221> CDS
 <222> (1)..(717)
 <220>
 <221> mat_peptide
 <222> (61)..()
 <400> 44

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Met	Arg	Phe	Ser	Ala	Gln	Leu	Leu	Gly	Leu	Leu	Val	Leu	Trp	Ile	Pro	
-20				-15				-10							-5	
gga	tcc	act	gca	gac	atc	gtg	atg	acc	cag	tct	gca	ctc	tcc	aat	cca	96
Gly	Ser	Thr	Ala	Asp	Ile	Val	Met	Thr	Gln	Ser	Ala	Leu	Ser	Asn	Pro	
	-1	1					5				10					
gtc	act	cct	gga	gag	ccg	ggt	tcc	atc	tcc	tgc	cgg	tct	agt	aag	agt	144
Val	Thr	Pro	Gly	Glu	Pro	Gly	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Lys	Ser	
	15					20					25					
ctc	cta	cat	agt	aat	ggc	atc	act	tat	ttg	tat	tgg	tat	ctg	cag	aaa	192
Leu	Leu	His	Ser	Asn	Gly	Ile	Thr	Tyr	Leu	Tyr	Trp	Tyr	Leu	Gln	Lys	
	30				35				40							
cca	ggg	cag	tct	cct	cag	ctg	ctc	atc	tat	cag	atg	tct	aac	aga	gcc	240
Pro	Gly	Gln	Ser	Pro	Gln	Leu	Leu	Ile	Tyr	Gln	Met	Ser	Asn	Arg	Ala	
45				50				55						60		
tca	ggg	gtc	cca	gac	agg	ttc	agt	agc	agt	gga	tct	ggg	aca	gat	ttc	288
Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Ser	Ser	Gly	Ser	Gly	Thr	Asp	Phe	
			65					70					75			
act	ctc	aag	atc	agc	aga	gtg	gag	gct	gaa	gat	gtg	gga	gtt	tat	tac	336
Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	
		80					85				90					
tgt	gct	cag	aac	cta	gag	ctt	ccg	cgg	acg	ttc	ggg	cag	ggc	acc	aag	384
Cys	Ala	Gln	Asn	Leu	Glu	Leu	Pro	Arg	Thr	Phe	Gly	Gln	Gly	Thr	Lys	
	95					100					105					
ctt	gag	atg	aaa	cga	act	gtg	gct	gca	cca	tct	gtc	tct	atc	ttc	ccg	432
Leu	Glu	Met	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	
	110				115						120					
cca	tct	gat	gag	cag	ttg	aaa	tct	gga	act	gcc	tct	gtt	gtg	tgc	ctg	480
Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	
125				130						135				140		
ctg	aat	aac	ttc	tat	ccc	aga	gag	gcc	aaa	gta	cag	tgg	aag	gtg	gat	528
Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	
			145					150					155			
aac	gcc	ctc	caa	tcg	ggt	aac	tcc	cag	gag	agt	gtc	aca	gag	cag	gac	576
Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	

160										165										170																				
agc	aag	gac	agc	acc	tac	agc	ctc	agc	agc	acc	ctg	acg	ctg	agc	aaa					agc	aag	gac	agc	acc	tac	agc	ctc	agc	agc	acc	ctg	acg	ctg	agc	aaa					624
Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys					Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys					
175										180										185																				
gca	gac	tac	gag	aaa	cac	aaa	gtc	tac	gcc	tgc	gaa	gtc	acc	cat	cag					gca	gac	tac	gag	aaa	cac	aaa	gtc	tac	gcc	tgc	gaa	gtc	acc	cat	cag					672
Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln					Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln					
190										195										200																				
ggc	ctg	agc	tcg	ccc	gtc	aca	aag	agc	ttc	aac	agg	gga	gag	tgt	tag					ggc	ctg	agc	tcg	ccc	gtc	aca	aag	agc	ttc	aac	agg	gga	gag	tgt	tag					720
Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys					Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys							
205										210										215																				

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<211> 239
<212> PRT
<213> Homo sapiens
<400> 45
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Gly	Ser	Thr	Ala	Asp	Ile	Val	Met	Thr	Gln	Ser	Ala	Leu	Ser	Asn	Pro
		-1	1				5						10		
Val	Thr	Pro	Gly	Glu	Pro	Gly	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Lys	Ser
		15				20						25			
Leu	Leu	His	Ser	Asn	Gly	Ile	Thr	Tyr	Leu	Tyr	Trp	Trp	Leu	Gln	Lys
30					35						40				
Pro	Gly	Gln	Ser	Pro	Gln	Leu	Leu	Ile	Tyr	Gln	Met	Ser	Asn	Arg	Ala
45					50					55					60
Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Ser	Ser	Gly	Ser	Gly	Thr	Asp	Phe
				65					70					75	
Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr
			80					85					90		
Cys	Ala	Gln	Asn	Leu	Glu	Leu	Pro	Arg	Thr	Phe	Gly	Gln	Gly	Thr	Lys
		95				100						105			
Leu	Glu	Met	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro
	110				115						120				
Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu
125					130					135					140
Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp
				145					150					155	
Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp
		160						165					170		
Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys
		175					180					185			
Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln
	190					195					200				
Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys	
205					210					215					

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<210> 46
<211> 85
<212> DNA
<213> Homo Sapiens
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<221> misc_feature
<223> P1 Oligo Human Engineered ING-1 with proline oligos
<400> 46
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actcttacta gaccggcagg agatggaacc tgactctccc agagtgactg gattggagag 60
tggagactqg gtcatcacga tgtct 85

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<210> 47
<211> 85
<212> DNA
<213> Homo Sapiens
<220>
<221> misc_feature
<223> P2 Oligo Human Engineered ING-1 with proline oligos
<400> 47
actcttacta gaccggcagg agatggaacc tgactctcca ggagtgactg gattggagag 60
tcgagactgg gtcatcacga tgtct 85

<210> 48
<211> 85
<212> DNA
<213> Homo Sapiens
<220>
<221> misc_feature
<223> P3 Oligo Human Engineered ING-1 with proline oligos
<400> 48
actcttacta gaccggcagg agatggaacc cggctctccc agagtgactg gattggagag 60
tcgagactgg gtcatcacga tgtct 85

<210> 49
<211> 85
<212> DNA
<213> Homo Sapiens
<220>
<221> misc_feature
<223> P1P2 Oligo Human Engineered ING-1 with proline oligos
<400> 49
actcttacta gaccggcagg agatggaacc cggctctcca ggagtgactg gattggagag 60
tcgagactgg gtcatcacga tgtct 85

<210> 50
<211> 85
<212> DNA
<213> Homo Sapiens
<220>
<221> misc_feature
<223> P1P3 Oligo Human Engineered ING-1 with proline oligos
<400> 50
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tggagactgg gtcatcacga tgtct 85

<210> 51
<211> 85
<212> DNA
<213> Homo Sapiens
<220>
<221> misc_feature
<223> P2P3 Oligo Human Engineered ING-1 with proline oligos
<400> 51
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tcgagactgg gtcatcacga tgtct 85

<210> 52

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<211> 19
 <212> DNA
 <213> Homo Sapiens
 <220>
 <221> misc_feature
 <223> Reverse Primer KBsr ING-1 Light Chain
 <400> 52
 cttactagac cggcaggag

19

<210> 53
 <211> 798
 <212> DNA
 <213> Homo sapiens
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 <221> misc_feature
 <223> EpCam truncated sequence
 <220>
 <221> CDS
 <222> (1)..(795)
 <400> 53

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Met	Ala	Pro	Pro	Gln	Val	Leu	Ala	Phe	Gly	Leu	Leu	Leu	Ala	Ala	Ala	
1			5					10					15			
acg	gcg	act	ttt	gcc	gca	gct	cag	gaa	gaa	tgt	gtc	tgt	gaa	aac	tac	96
Thr	Ala	Thr	Phe	Ala	Ala	Ala	Gln	Glu	Cys	Val	Cys	Gln	Asn	Tyr		
			20				25					30				
aag	ctg	gcc	gta	aac	tgc	ttt	gtg	aat	aat	aat	cgt	caa	tgc	cag	tgt	144
Lys	Leu	Ala	Val	Asn	Cys	Phe	Val	Asn	Asn	Asn	Arg	Gln	Cys	Gln	Cys	
			35				40				45					
act	tca	gtt	ggg	gca	caa	aat	act	gtc	att	tgc	tca	aag	ctg	gct	gcc	192
Thr	Ser	Val	Gly	Ala	Gln	Asn	Thr	Val	Ile	Cys	Ser	Lys	Leu	Ala	Ala	
			50				55				60					
aaa	tgt	ttg	gtg	atg	aag	gca	gaa	atg	aat	ggc	tca	aaa	ctt	ggg	aga	240
Lys	Cys	Leu	Val	Met	Lys	Ala	Glu	Met	Asn	Gly	Ser	Lys	Leu	Gly	Arg	
65				70				75				80				
aga	gca	aaa	cct	gaa	ggg	gcc	ctc	cag	aac	aat	gat	ggg	ctt	tat	gat	288
Arg	Ala	Lys	Pro	Glu	Gly	Ala	Leu	Gln	Asn	Asp	Gly	Leu	Tyr	Asp		
			85				90					95				
cct	gac	tgc	gat	gag	agc	ggg	ctc	ttt	aag	gcc	aag	cag	tgc	aac	ggc	336
Pro	Asp	Cys	Asp	Glu	Ser	Gly	Leu	Phe	Lys	Ala	Lys	Gln	Cys	Asn	Gly	
			100				105					110				
acc	tcc	acg	tgc	tgg	tgt	gtg	aac	act	gct	ggg	gtc	aga	acc	aca	gac	384
Thr	Ser	Thr	Cys	Trp	Cys	Val	Asn	Thr	Ala	Gly	Val	Arg	Arg	Thr	Asp	
			115				120					125				
aag	gac	act	gaa	ata	acc	tgc	tct	gag	cga	gtg	aga	acc	tac	tgg	atc	432
Lys	Asp	Thr	Glu	Ile	Thr	Cys	Ser	Glu	Arg	Val	Arg	Thr	Tyr	Trp	Ile	
			130				135				140					
atc	att	gaa	cta	aaa	cac	aaa	gca	aga	gaa	aaa	cct	tat	gat	agt	aaa	480
Ile	Ile	Glu	Leu	Lys	His	Lys	Ala	Arg	Glu	Lys	Pro	Tyr	Asp	Ser	Lys	
145				150				155				160				
agt	ttg	cgg	act	gca	ctt	cag	aag	gag	atc	aca	acg	cgt	tat	caa	ctg	528
Ser	Leu	Arg	Thr	Ala	Leu	Gln	Lys	Glu	Ile	Thr	Thr	Arg	Tyr	Gln	Leu	
				165				170				175				
gat	cca	aaa	ttt	atc	acg	agt	att	ttg	tat	gag	aat	aat	gtt	atc	act	576
Asp	Pro	Lys	Phe	Ile	Thr	Ser	Ile	Leu	Tyr	Glu	Asn	Asn	Val	Ile	Thr	
			180					185				190				
att	gat	ctg	ggt	caa	aat	tct	tct	caa	aaa	act	cag	aat	gat	gtg	gac	624

Ile	Asp	Leu	Val	Gln	Asn	Ser	Ser	Gln	Lys	Thr	Gln	Asn	Asp	Val	Asp		
		195					200					205					
ata	gct	gat	gtg	gct	tat	tat	ttt	gaa	aaa	gat	ggt	aaa	ggg	gaa	tcc		672
Ile	Ala	Asp	Val	Ala	Tyr	Tyr	Phe	Glu	Lys	Asp	Val	Lys	Gly	Glu	Ser		
		210					215					220					
ttg	ttt	cat	tct	aag	aaa	atg	gac	ctg	aca	gta	aat	ggg	gaa	caa	ctg		720
Leu	Phe	His	Ser	Lys	Lys	Met	Asp	Leu	Thr	Val	Asn	Gly	Glu	Gln	Leu		
		225				230				235					240		
gat	ctg	gat	cct	ggg	caa	act	tta	att	tat	tat	ggt	gat	gaa	aaa	gca		768
Asp	Leu	Asp	Pro	Gly	Gln	Thr	Leu	Ile	Tyr	Tyr	Val	Asp	Glu	Lys	Ala		
				245					250					255			
cct	gaa	ttc	tca	atg	cag	ggg	cta	aaa	taa								798
Pro	Glu	Phe	Ser	Met	Gln	Gly	Leu	Lys									
				260				265									

<210> 54

<211> 265

<212> PRT

<213> Homo sapiens

<400> 54

Met	Ala	Pro	Pro	Gln	Val	Leu	Ala	Phe	Gly	Leu	Leu	Leu	Ala	Ala	Ala		
				5					10					15			
Thr	Ala	Thr	Phe	Ala	Ala	Gln	Glu	Glu	Cys	Val	Cys	Glu	Asn	Tyr			
			20				25					30					
Lys	Leu	Ala	Val	Asn	Cys	Phe	Val	Asn	Asn	Arg	Gln	Cys	Gln	Cys			
		35				40					45						
Thr	Ser	Val	Gly	Ala	Gln	Asn	Thr	Val	Ile	Cys	Ser	Lys	Leu	Ala	Ala		
		50			55						60						
Lys	Cys	Leu	Val	Met	Lys	Ala	Glu	Met	Asn	Gly	Ser	Lys	Leu	Gly	Arg		
		65			70					75				80			
Arg	Ala	Lys	Pro	Glu	Gly	Ala	Leu	Gln	Asn	Asn	Asp	Gly	Leu	Tyr	Asp		
			85						90					95			
Pro	Asp	Cys	Asp	Glu	Ser	Gly	Leu	Phe	Lys	Ala	Lys	Gln	Cys	Asn	Gly		
			100					105					110				
Thr	Ser	Thr	Cys	Trp	Cys	Val	Asn	Thr	Ala	Gly	Val	Arg	Arg	Thr	Asp		
		115					120					125					
Lys	Asp	Thr	Glu	Ile	Thr	Cys	Ser	Glu	Arg	Val	Arg	Thr	Tyr	Trp	Ile		
		130				135					140						
Ile	Ile	Glu	Leu	Lys	His	Lys	Ala	Arg	Glu	Lys	Pro	Tyr	Asp	Ser	Lys		
		145			150					155				160			
Ser	Leu	Arg	Thr	Ala	Leu	Gln	Lys	Glu	Ile	Thr	Thr	Arg	Tyr	Gln	Leu		
			165						170					175			
Asp	Pro	Lys	Phe	Ile	Thr	Ser	Ile	Leu	Tyr	Glu	Asn	Asn	Val	Ile	Thr		
			180					185					190				
Ile	Asp	Leu	Val	Gln	Asn	Ser	Ser	Gln	Lys	Thr	Gln	Asn	Asp	Val	Asp		
		195					200					205					
Ile	Ala	Asp	Val	Ala	Tyr	Tyr	Phe	Glu	Lys	Asp	Val	Lys	Gly	Glu	Ser		
		210				215					220						
Leu	Phe	His	Ser	Lys	Lys	Met	Asp	Leu	Thr	Val	Asn	Gly	Glu	Gln	Leu		
		225			230					235				240			
Asp	Leu	Asp	Pro	Gly	Gln	Thr	Leu	Ile	Tyr	Tyr	Val	Asp	Glu	Lys	Ala		
				245					250					255			
Pro	Glu	Phe	Ser	Met	Gln	Gly	Leu	Lys									
				260				265									

<210> 55

<211> 945

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<212> DNA
<213> Homo sapiens
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<221> misc_feature
<223> Full-Length EpCam
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<221> CDS
<222> (1)..(942)
<220>
<221> mat_peptide
<222> (70)..()
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Met Ala Pro Pro Gln Val Leu Ala Phe Gly Leu Leu Leu Ala Ala Ala
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acg gcg act ttt gcc gca gct cag gaa gaa tgt gtc tgt gaa aac tac      96
Thr Ala Thr Phe Ala Ala Ala Gln Glu Glu Cys Val Cys Glu Asn Tyr
-5 -1 1 5
aag ctg gcc gta aac tgc ttt gtg aat aat aat cgt caa tgc cag tgt      144
Lys Leu Ala Val Asn Cys Phe Val Asn Asn Asn Arg Gln Cys Gln Cys
10 15 20 25
act tca gtt ggt gca caa aat act gtc att tgc tca aag ctg gct gcc      192
Thr Ser Val Gly Ala Gln Asn Thr Val Ile Cys Ser Lys Leu Ala Ala
30 35 40
aaa tgt ttg gtg atg aag gca gaa atg aat ggc tca aaa ctt ggg aga      240
Lys Cys Leu Val Met Lys Ala Glu Met Asn Gly Ser Lys Leu Gly Arg
45 50 55
aga gca aaa cct gaa ggg gcc ctc cag aac aat gat ggg ctt tat gat      288
Arg Ala Lys Pro Glu Gly Ala Leu Gln Asn Asn Asp Gly Leu Tyr Asp
60 65 70
cct gac tgc gat gag agc ggg ctc ttt aag gcc aag cag tgc aac ggc      336
Pro Asp Cys Asp Glu Ser Gly Leu Phe Lys Ala Lys Gln Cys Asn Gly
75 80 85
acc tcc acg tgc tgg tgt gtg aac act gct ggg gtc aga aga aca gac      384
Thr Ser Thr Cys Trp Cys Val Asn Thr Ala Gly Val Arg Arg Thr Asp
90 95 100 105
aag gac act gaa ata acc tgc tct gag cga gtg aga acc tac tgg atc      432
Lys Asp Thr Glu Ile Thr Cys Ser Glu Arg Val Arg Thr Tyr Trp Ile
110 115 120
atc att gaa cta aaa cac aaa gca aga gaa aaa cct tat gat agt aaa      480
Ile Ile Glu Leu Lys His Lys Ala Arg Glu Lys Pro Tyr Asp Ser Lys
125 130 135
agt ttg cgg act gca ctt cag aag gag atc aca acg cgt tat caa ctg      528
Ser Leu Arg Thr Ala Leu Gln Lys Glu Ile Thr Thr Arg Tyr Gln Leu
140 145 150
gat cca aaa ttt atc acg agt att ttg tat gag aat aat gtt atc act      576
Asp Pro Lys Phe Ile Thr Ser Ile Leu Tyr Glu Asn Asn Val Ile Thr
155 160 165
att gat ctg gtt caa aat tct tct caa aaa act cag aat gat gtg gac      624
Ile Asp Leu Val Gln Asn Ser Ser Gln Lys Thr Gln Asn Asp Val Asp
170 175 180 185
ata gct gat gtg gct tat tat ttt gaa aaa gat gtt aaa ggt gaa tcc      672
Ile Ala Asp Val Ala Tyr Tyr Phe Glu Lys Asp Val Lys Gly Glu Ser
190 195 200
ttg ttt cat tct aag aaa atg gac ctg aca gta aat ggg gaa caa ctg      720
Leu Phe His Ser Lys Lys Met Asp Leu Thr Val Asn Gly Glu Gln Leu
205 210 215

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gat	ctg	gat	cct	ggg	caa	act	tta	att	tat	tat	gtt	gat	gaa	aaa	gca	768
Asp	Leu	Asp	Pro	Gly	Gln	Thr	Leu	Ile	Tyr	Tyr	Val	Asp	Glu	Lys	Ala	
	220						225				230					
cct	gaa	ttc	tca	atg	cag	ggg	cta	aaa	gct	ggg	gtt	att	gct	gtt	att	816
Pro	Glu	Phe	Ser	Met	Gln	Gly	Leu	Lys	Ala	Gly	Val	Ile	Ala	Val	Ile	
	235					240				245						
gtg	gtt	gtg	gtg	ata	gca	gtt	gtt	gct	gga	att	gtt	gtg	ctg	gtt	att	864
Val	Val	Val	Val	Ile	Ala	Val	Val	Ala	Gly	Ile	Val	Val	Leu	Val	Ile	
	250				255				260						265	
tcc	aga	aag	aag	aga	atg	gca	aag	tat	gag	aag	gct	gag	ata	aag	gag	912
Ser	Arg	Lys	Lys	Arg	Met	Ala	Lys	Tyr	Glu	Lys	Ala	Glu	Ile	Lys	Glu	
				270					275					280		
atg	ggg	gag	atg	cat	agg	gaa	ctc	aat	gca	taa						945
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			285					290								

<210> 56

<211> 314

<212> PRT

<213> Homo sapiens

<400> 56

Met	Ala	Pro	Pro	Gln	Val	Leu	Ala	Phe	Gly	Leu	Leu	Leu	Ala	Ala	Ala	
			-20					-15					-10			
Thr	Ala	Thr	Phe	Ala	Ala	Ala	Gln	Glu	Glu	Cys	Val	Cys	Glu	Asn	Tyr	
		-5				-1	1				5					
Lys	Leu	Ala	Val	Asn	Cys	Phe	Val	Asn	Asn	Asn	Arg	Gln	Cys	Gln	Cys	
	10			15					20				25			
Thr	Ser	Val	Gly	Ala	Gln	Asn	Thr	Val	Ile	Cys	Ser	Lys	Leu	Ala	Ala	
			30					35					40			
Lys	Cys	Leu	Val	Met	Lys	Ala	Glu	Met	Asn	Gly	Ser	Lys	Leu	Gly	Arg	
		45					50					55				
Arg	Ala	Lys	Pro	Glu	Gly	Ala	Leu	Gln	Asn	Asn	Asp	Gly	Leu	Tyr	Asp	
	60					65					70					
Pro	Asp	Cys	Asp	Glu	Ser	Gly	Leu	Phe	Lys	Ala	Lys	Gln	Cys	Asn	Gly	
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Thr	Ser	Thr	Cys	Trp	Cys	Val	Asn	Thr	Ala	Gly	Val	Arg	Arg	Thr	Asp	
	90				95					100					105	
Lys	Asp	Thr	Glu	Ile	Thr	Cys	Ser	Glu	Arg	Val	Arg	Thr	Tyr	Trp	Ile	
			110						115					120		
Ile	Ile	Glu	Leu	Lys	His	Lys	Ala	Arg	Glu	Lys	Pro	Tyr	Asp	Ser	Lys	
		125					130						135			
Ser	Leu	Arg	Thr	Ala	Leu	Gln	Lys	Glu	Ile	Thr	Thr	Arg	Tyr	Gln	Leu	
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Asp	Pro	Lys	Phe	Ile	Thr	Ser	Ile	Leu	Tyr	Glu	Asn	Asn	Val	Ile	Thr	
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Ile	Asp	Leu	Val	Gln	Asn	Ser	Ser	Gln	Lys	Thr	Gln	Asn	Asp	Val	Asp	
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Ile	Ala	Asp	Val	Ala	Tyr	Tyr	Phe	Glu	Lys	Asp	Val	Lys	Gly	Glu	Ser	
			190						195					200		
Leu	Phe	His	Ser	Lys	Lys	Met	Asp	Leu	Thr	Val	Asn	Gly	Glu	Gln	Leu	
			205				210					215				
Asp	Leu	Asp	Pro	Gly	Gln	Thr	Leu	Ile	Tyr	Val	Asp	Glu	Lys	Lys	Ala	
	220						225				230					
Pro	Glu	Phe	Ser	Met	Gln	Gly	Leu	Lys	Ala	Gly	Val	Ile	Ala	Val	Ile	
	235				240					245						
Val	Val	Val	Val	Ile	Ala	Val	Val	Ala	Gly	Ile	Val	Val	Leu	Val	Ile	
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